

SEQUENCE LISTING

<110> KAO CORPORATION

<120> Alkaline Protease

<130> FP-KS-0498

<150> JP 09-274570

<151> 1997-10-07

<160> 5

<210> 1

<211> 639

<212> PRT

<213> *Bacillus sp.*

<220>

<221> misc__feature

<222> 23, 29, 32, 46, 47, 53, 70, 74, 89, 102, 105, 128, 130, 131, 132, 133, 146,
148, 160, 165, 172, 183, 187, 188, 189, 194, 286, 306, 324, 369, 431, 501,
531, 541, 584, 591, 592, 594, 595, 596, 611, 632

<223> Xaa=arbitraty amino acid

<400>

Met	Arg	Lys	Lys	Lys	Val	Phe	Leu	Ser	Val	Leu	Ser	Ala	Ala	Ala	Ile
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			20					25					30		
Phe	Asp	Leu	Asp	Phe	Lys	Gly	Ile	Gln	Thr	Thr	Thr	Asp	Xaa	Xaa	Gly
		35					40					45			
Phe	Ser	Lys	Gln	Xaa	Gln	Thr	Gly	Ala	Ala	Ala	Phe	Leu	Val	Glu	Ser
	50				55						60				
Glu	Asn	Val	Lys	Leu	Xaa	Lys	Gly	Leu	Xaa	Lys	Lys	Leu	Glu	Thr	Val
65			70					75				80			
Pro	Ala	Asn	Asn	Lys	Leu	His	Ile	Xaa	Gln	Phe	Asn	Gly	Pro	Ile	Leu
			85					90				95			
Glu	Glu	Thr	Lys	Gln	Xaa	Leu	Glu	Xaa	Thr	Gly	Ala	Lys	Ile	Leu	Asp
			100					105				110			
Tyr	Ile	Pro	Asp	Tyr	Ala	Tyr	Ile	Val	Glu	Tyr	Glu	Gly	Asp	Val	Xaa
		115					120					125			
Ser	Xaa	Xaa	Xaa	Xaa	Ile	Glu	His	Val	Glu	Ser	Val	Glu	Pro	Tyr	Leu
	130				135							140			
Pro	Xaa	Tyr	Xaa	Ile	Asp	Pro	Gln	Leu	Phe	Thr	Lys	Gly	Ala	Ser	Xaa
145				150					155					160	
Leu	Val	Lys	Ala	Xaa	Ala	Leu	Asp	Thr	Lys	Gln	Xaa	Asn	Lys	Glu	Val
			165					170				175			
Gln	Leu	Arg	Gly	Ile	Glu	Xaa	Ile	Ala	Gln	Xaa	Xaa	Xaa	Ser	Asn	Asp
		180						185				190			
Val	Xaa	Tyr	Ile	Thr	Ala	Lys	Pro	Glu	Tyr	Lys	Val	Met	Asn	Asp	Val
		195						200				205			

Ala Arg Gly Ile Val Lys Ala Asp Val Ala Gln Ser Ser Tyr Gly Leu
 210 215 220
 Tyr Gly Gln Gly Gln Ile Val Ala Val Ala Asp Thr Gly Leu Asp Thr
 225 230 235 240
 Gly Arg Asn Asp Ser Ser Met His Glu Ala Phe Arg Gly Lys Ile Thr
 245 250 255
 Ala Leu Tyr Ala Leu Gly Arg Thr Asn Asn Ala Asn Asp Thr Asn Gly
 260 265 270
 His Gly Thr His Val Ala Gly Ser Val Leu Gly Asn Gly Xaa Thr Asn
 275 280 285
 Lys Gly Met Ala Pro Gln Ala Asn Leu Val Phe Gln Ser Ile Met Asp
 290 295 300
 Ser Xaa Gly Gly Leu Gly Gly Leu Pro Ser Asn Leu Gln Thr Leu Phe
 305 310 315 320
 Ser Gln Ala Xaa Ser Ala Gly Ala Arg Ile His Thr Asn Ser Trp Gly
 325 330 335
 Ala Ala Val Asn Gly Ala Tyr Thr Thr Asp Ser Arg Asn Val Asp Asp
 340 345 350
 Tyr Val Arg Lys Asn Asp Met Thr Ile Leu Phe Ala Ala Gly Asn Glu
 355 360 365
 Xaa Pro Asn Gly Gly Thr Ile Ser Ala Pro Gly Thr Ala Lys Asn Ala
 370 375 380
 Ile Thr Val Gly Ala Thr Glu Asn Leu Arg Pro Ser Phe Gly Ser Tyr
 385 390 395 400
 Ala Asp Asn Ile Asn His Val Ala Gln Phe Ser Ser Arg Gly Pro Thr
 405 410 415

Lys	Asp	Gly	Arg	Ile	Lys	Pro	Asp	Val	Met	Ala	Pro	Gly	Thr	Xaa	Ile
					420					425					430
Leu	Ser	Ala	Arg	Ser	Ser	Leu	Ala	Pro	Asp	Ser	Ser	Phe	Trp	Ala	Asn
					435					440					445
His	Asp	Ser	Lys	Tyr	Ala	Tyr	Met	Gly	Gly	Thr	Ser	Met	Ala	Thr	Pro
					450					455					460
Ile	Val	Ala	Gly	Asn	Val	Ala	Gln	Leu	Arg	Glu	His	Phe	Val	Lys	Asn
465					470					475					480
Arg	Gly	Ile	Thr	Pro	Lys	Pro	Ser	Leu	Leu	Lys	Ala	Ala	Leu	Ile	Ala
					485					490					495
Gly	Ala	Ala	Asp	Xaa	Gly	Leu	Gly	Tyr	Pro	Asn	Gly	Asn	Gln	Gly	Trp
					500					505					510
Gly	Arg	Val	Thr	Leu	Asp	Lys	Ser	Leu	Asn	Val	Ala	Tyr	Val	Asn	Glu
					515					520					525
Ser	Ser	Xaa	Leu	Ser	Thr	Ser	Gln	Lys	Ala	Thr	Tyr	Xaa	Phe	Thr	Ala
					530					535					540
Thr	Ala	Gly	Lys	Pro	Leu	Lys	Ile	Ser	Leu	Val	Trp	Ser	Asp	Ala	Pro
545					550					555					560
Ala	Ser	Thr	Thr	Ala	Ser	Val	Thr	Leu	Val	Asn	Asp	Leu	Asp	Leu	Val
					565					570					575
Ile	Thr	Ala	Pro	Asn	Gly	Thr	Xaa	Tyr	Val	Gly	Asn	Asp	Phe	Xaa	Xaa
					580					585					590
Pro	Xaa	Xaa	Xaa	Asn	Trp	Asp	Gly	Arg	Asn	Asn	Val	Glu	Asn	Val	Phe
					595					600					605
Ile	Asn	Xaa	Pro	Gln	Ser	Gly	Thr	Tyr	Thr	Ile	Glu	Val	Gln	Ala	Tyr
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Asn Val Pro Val Gly Pro Gln Xaa Phe Ser Leu Ala Ile Val Asn

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630

635

<210> 2

<211> 640

<212> PRT

<213> *Bacillus sp.*

<220>

<221> misc_feature

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149, 161, 166, 173, 184, 188, 189, 190, 195, 287, 307, 325, 370, 432, 502,
532, 542, 585, 592, 593, 595, 596, 597, 612, 633

<223> Xaa=arbitrary amino acid

<400>

Met Arg Xaa Lys Lys Lys Val Phe Leu Ser Val Leu Ser Ala Ala Ala

1

5

10

15

Ile Leu Ser Thr Val Ala Leu Xaa Asn Pro Ser Ala Gly Xaa Ala Arg

20

25

30

Xaa Phe Asp Leu Asp Phe Lys Gly Ile Gln Thr Thr Thr Asp Xaa Xaa

35

40

45

Gly Phe Ser Lys Gln Xaa Gln Thr Gly Ala Ala Ala Phe Leu Val Glu

50

55

60

Ser Glu Asn Val Lys Leu Xaa Lys Gly Leu Xaa Lys Lys Leu Glu Thr

65

70

75

80

Val Pro Ala Asn Asn Lys Leu His Ile Xaa Gln Phe Asn Gly Pro Ile

85	90	95
Leu Glu Glu Thr Lys Gln Xaa	Leu Glu Xaa Thr Gly Ala Lys	Ile Leu
100	105	110
Asp Tyr Ile Pro Asp Tyr Ala Tyr	Ile Val Glu Tyr Glu Gly Asp	Val
115	120	125
Xaa Ser Xaa Xaa Xaa Xaa Ile Glu His	Val Glu Ser Val Glu Pro Tyr	
130	135	140
Leu Pro Xaa Tyr Xaa Ile Asp Pro Gln	Leu Phe Thr Lys Gly Ala Ser	
145	150	155
Xaa Leu Val Lys Ala Xaa Ala Leu Asp	Thr Lys Gln Xaa Asn Lys Glu	
165	170	175
Val Gln Leu Arg Gly Ile Glu Xaa Ile	Ala Gln Xaa Xaa Xaa Ser Asn	
180	185	190
Asp Val Xaa Tyr Ile Thr Ala Lys Pro	Glu Tyr Lys Val Met Asn Asp	
195	200	205
Val Ala Arg Gly Ile Val Lys Ala Asp	Val Ala Gln Ser Ser Tyr Gly	
210	215	220
Leu Tyr Gly Gln Gly Gln Ile Val Ala	Val Ala Asp Thr Gly Leu Asp	
225	230	235
Thr Gly Arg Asn Asp Ser Ser Met His	Glu Ala Phe Arg Gly Lys Ile	
245	250	255
Thr Ala Leu Tyr Ala Leu Gly Arg Thr	Asn Asn Ala Asn Asp Thr Asn	
260	265	270
Gly His Gly Thr His Val Ala Gly Ser	Val Leu Gly Asn Gly Xaa Thr	
275	280	285
Asn Lys Gly Met Ala Pro Gln Ala Asn	Leu Val Phe Gln Ser Ile Met	

290	295	300	
Asp Ser Xaa Gly Gly Leu Gly Gly Leu Pro Ser Asn Leu Gln Thr Leu			
305	310	315	320
Phe Ser Gln Ala Xaa Ser Ala Gly Ala Arg Ile His Thr Asn Ser Trp			
	325	330	335
Gly Ala Ala Val Asn Gly Ala Tyr Thr Thr Asp Ser Arg Asn Val Asp			
	340	345	350
Asp Tyr Val Arg Lys Asn Asp Met Thr Ile Leu Phe Ala Ala Gly Asn			
	355	360	365
Glu Xaa Pro Asn Gly Gly Thr Ile Ser Ala Pro Gly Thr Ala Lys Asn			
	370	375	380
Ala Ile Thr Val Gly Ala Thr Glu Asn Leu Arg Pro Ser Phe Gly Ser			
385	390	395	400
Tyr Ala Asp Asn Ile Asn His Val Ala Gln Phe Ser Ser Arg Gly Pro			
	405	410	415
Thr Lys Asp Gly Arg Ile Lys Pro Asp Val Met Ala Pro Gly Thr Xaa			
	420	425	430
Ile Leu Ser Ala Arg Ser Ser Leu Ala Pro Asp Ser Ser Phe Trp Ala			
	435	440	445
Asn His Asp Ser Lys Tyr Ala Tyr Met Gly Gly Thr Ser Met Ala Thr			
	450	455	460
Pro Ile Val Ala Gly Asn Val Ala Gln Leu Arg Glu His Phe Val Lys			
465	470	475	480
Asn Arg Gly Ile Thr Pro Lys Pro Ser Leu Leu Lys Ala Ala Leu Ile			
	485	490	495
Ala Gly Ala Ala Asp Xaa Gly Leu Gly Tyr Pro Asn Gly Asn Gln Gly			

500	505	510
Trp Gly Arg Val Thr Leu Asp Lys Ser Leu Asn Val Ala Tyr Val Asn		
515	520	525
Glu Ser Ser Xaa Leu Ser Thr Ser Gln Lys Ala Thr Tyr Xaa Phe Thr		
530	535	540
Ala Thr Ala Gly Lys Pro Leu Lys Ile Ser Leu Val Trp Ser Asp Ala		
545	550	555
Pro Ala Ser Thr Thr Ala Ser Val Thr Leu Val Asn Asp Leu Asp Leu		
565	570	575
Val Ile Thr Ala Pro Asn Gly Thr Xaa Tyr Val Gly Asn Asp Phe Xaa		
580	585	590
Xaa Pro Xaa Xaa Xaa Asn Trp Asp Gly Arg Asn Asn Val Glu Asn Val		
595	600	605
Phe Ile Asn Xaa Pro Gln Ser Gly Thr Tyr Thr Ile Glu Val Gln Ala		
610	615	620
Tyr Asn Val Pro Val Gly Pro Gln Xaa Phe Ser Leu Ala Ile Val Asn		
625	630	635
		640

<210> 3

<211> 1920

<212> DNA

<213> *Bacillus sp.*

<400>

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ctg tcg act gtt gca tta aac aat ccc tcg gct ggt gat gca agg act	96			
Leu Ser Thr Val Ala Leu Asn Asn Pro Ser Ala Gly Asp Ala Arg Thr				
20	25	30		
ttt gat ctg gat ttt aaa gga att caa aca aca acc gat gtc agt ggt	144			
Phe Asp Leu Asp Phe Lys Gly Ile Gln Thr Thr Thr Asp Val Ser Gly				
35	40	45		
ttc tcc aaa cag cga caa aca ggt gcg gct gca ttt ctg gtg gag tct	192			
Phe Ser Lys Gln Arg Gln Thr Gly Ala Ala Ala Phe Leu Val Glu Ser				
50	55	60		
gaa aat gtg aaa ctt ctt aaa gga ttg cta aag aaa ctt gaa aca gta	240			
Glu Asn Val Lys Leu Leu Lys Gly Leu Leu Lys Lys Leu Glu Thr Val				
65	70	75	80	
ccg gca aat aat aaa ctc cat att gtc caa ttc aat ggc ccc att tta	288			
Pro Ala Asn Asn Lys Leu His Ile Val Gln Phe Asn Gly Pro Ile Leu				
85	90	95		
gaa gaa aca aaa cag aag cta gag aca act gga gca aag att ctc gac	336			
Glu Glu Thr Lys Gln Lys Leu Glu Thr Thr Gly Ala Lys Ile Leu Asp				
100	105	110		
tac atc cct gat tat gca tat att gtc gag tat gag ggg gat gtt cag	384			
Tyr Ile Pro Asp Tyr Ala Tyr Ile Val Glu Tyr Glu Gly Asp Val Gln				
115	120	125		
tca aaa gtc cgc tcc att gaa cac gtg gaa tca gtg gag cca tac ttg	432			
Ser Lys Val Arg Ser Ile Glu His Val Glu Ser Val Glu Pro Tyr Leu				
130	135	140		
ccg aaa tac aaa ata gat ccc cag ctt ttc aca aaa ggc gca tcg acg	480			

Pro Lys Tyr Lys Ile Asp Pro Gln Leu Phe Thr Lys Gly Ala Ser Thr
 145 150 155 160
 ctg gtg aaa gcg ttg gcg ctt gat acg aag cag aac aat aaa gaa gtg 528
 Leu Val Lys Ala Leu Ala Leu Asp Thr Lys Gln Asn Asn Lys Glu Val
 165 170 175
 caa tta aga ggc atc gag gaa atc gct cag tac gta gca agc aat gac 576
 Gln Leu Arg Gly Ile Glu Glu Ile Ala Gln Tyr Val Ala Ser Asn Asp
 180 185 190
 gtc cat tat att acg gca aag cct gaa tat aag gtg atg aat gat gtg 624
 Val His Tyr Ile Thr Ala Lys Pro Glu Tyr Lys Val Met Asn Asp Val
 195 200 205
 gcc aga ggt att gtc aaa gcg gat gtg gca cag agc agc tac ggt ttg 672
 Ala Arg Gly Ile Val Lys Ala Asp Val Ala Gln Ser Ser Tyr Gly Leu
 210 215 220
 tat gga caa ggc cag att gtc gca gtt gcc gat act gga ttg gat aca 720
 Tyr Gly Gln Gly Gln Ile Val Ala Val Ala Asp Thr Gly Leu Asp Thr
 225 230 235 240
 gga aga aac gac agt tcg atg cat gaa gcc ttc cgc ggt aaa ata aca 768
 Gly Arg Asn Asp Ser Ser Met His Glu Ala Phe Arg Gly Lys Ile Thr
 245 250 255
 gca cta tat gca ctg ggt cgg acg aat aat gcg aat gat acg aac ggt 816
 Ala Leu Tyr Ala Leu Gly Arg Thr Asn Asn Ala Asn Asp Thr Asn Gly
 260 265 270
 cat ggt acc cat gtg gca ggt tcg gta tta gga aat ggc gca acg aat 864
 His Gly Thr His Val Ala Gly Ser Val Leu Gly Asn Gly Ala Thr Asn
 275 280 285

aaa gga atg gca cct caa gcg aat ctg gtt ttt caa tcc atc atg gat 912
 Lys Gly Met Ala Pro Gln Ala Asn Leu Val Phe Gln Ser Ile Met Asp
 290 295 300
 agc agt ggt ggg ctt gga ggc ttg cct tcc aat ctg caa acc tta ttc 960
 Ser Ser Gly Gly Leu Gly Gly Leu Pro Ser Asn Leu Gln Thr Leu Phe
 305 310 315 320
 agc caa gca ttc agt gca ggt gcc aga att cat aca aac tcc tgg ggg 1008
 Ser Gln Ala Phe Ser Ala Gly Ala Arg Ile His Thr Asn Ser Trp Gly
 325 330 335
 gca gcg gtg aat ggg gcc tac acg aca gat tcc aga aat gtg gat gac 1056
 Ala Ala Val Asn Gly Ala Tyr Thr Thr Asp Ser Arg Asn Val Asp Asp
 340 345 350
 tat gta agg aaa aat gat atg acg att ctt ttc gcg gct ggg aat gaa 1104
 Tyr Val Arg Lys Asn Asp Met Thr Ile Leu Phe Ala Ala Gly Asn Glu
 355 360 365
 agg ccg aac ggc ggt acc atc agt gca cct ggt acg gct aaa aac gcc 1152
 Arg Pro Asn Gly Gly Thr Ile Ser Ala Pro Gly Thr Ala Lys Asn Ala
 370 375 380
 ata aca gtc ggc gca acc gaa aac ctg cgt cca agc ttc ggt tcc tat 1200
 Ile Thr Val Gly Ala Thr Glu Asn Leu Arg Pro Ser Phe Gly Ser Tyr
 385 390 395 400
 gca gat aat att aac cac gtt gca cag ttc tct tcc cgt ggc ccg aca 1248
 Ala Asp Asn Ile Asn His Val Ala Gln Phe Ser Ser Arg Gly Pro Thr
 405 410 415
 aaa gat ggg cga atc aag cct gat gtc atg gcg cca ggg aca tac att 1296
 Lys Asp Gly Arg Ile Lys Pro Asp Val Met Ala Pro Gly Thr Tyr Ile

420	425	430	
tta tca gca aga tct tct ctt gca ccc gat tcc tcc ttc tgg gcg aat 1344			
Leu Ser Ala Arg Ser Ser Leu Ala Pro Asp Ser Ser Phe Trp Ala Asn			
435	440	445	
cat gac agc aaa tat gcc tat atg ggt gga acg tcc atg gca aca ccg 1392			
His Asp Ser Lys Tyr Ala Tyr Met Gly Gly Thr Ser Met Ala Thr Pro			
450	455	460	
att gtt gcg ggg aat gtt gca cag ctc cgt gag cat ttt gtg aaa aat 1440			
Ile Val Ala Gly Asn Val Ala Gln Leu Arg Glu His Phe Val Lys Asn			
465	470	475	480
aga gga atc act cct aag cct tcc cta ttg aaa gca gct ttg att gca 1488			
Arg Gly Ile Thr Pro Lys Pro Ser Leu Leu Lys Ala Ala Leu Ile Ala			
485	490	495	
ggg gct gct gat gtt gga ttg ggt tat ccg aac gga aac caa gga tgg 1536			
Gly Ala Ala Asp Val Gly Leu Gly Tyr Pro Asn Gly Asn Gln Gly Trp			
500	505	510	
ggc cga gtg acc ctg gat aaa tcg ttg aac gtt gcc tat gtg aac gaa 1584			
Gly Arg Val Thr Leu Asp Lys Ser Leu Asn Val Ala Tyr Val Asn Glu			
515	520	525	
tcc agt gcc cta tca act agc caa aaa gcg aca tat acc ttt act gca 1632			
Ser Ser Ala Leu Ser Thr Ser Gln Lys Ala Thr Tyr Thr Phe Thr Ala			
530	535	540	
acg gcg ggc aag cca ttg aaa atc tcc ctg gta tgg tcg gat gcc cct 1680			
Thr Ala Gly Lys Pro Leu Lys Ile Ser Leu Val Trp Ser Asp Ala Pro			
545	550	555	560
gca agc act act gct tct gta acc ctg gtc aat gat ttg gat ttg gtc 1728			

Ala Ser Thr Thr Ala Ser Val Thr Leu Val Asn Asp Leu Asp Leu Val

565

570

575

att aca gca cca aac gga aca aga tat gtc ggg aat gac ttc tca gca 1776

Ile Thr Ala Pro Asn Gly Thr Arg Tyr Val Gly Asn Asp Phe Ser Ala

580

585

590

cca ttt gac aat aac tgg gat ggc cgc aat aac gta gaa aat gta ttt 1824

Pro Phe Asp Asn Asn Trp Asp Gly Arg Asn Asn Val Glu Asn Val Phe

595

600

605

att aat tcg ccc caa agt gga aca tat acc att gag gtg caa gca tat 1872

Ile Asn Ser Pro Gln Ser Gly Thr Tyr Thr Ile Glu Val Gln Ala Tyr

610

615

620

aat gtg ccg gtt gga cca caa aac ttc tcg ttg gca att gtg aac taa 1920

Asn Val Pro Val Gly Pro Gln Asn Phe Ser Leu Ala Ile Val Asn

625

630

635

<210> 4

<211> 1923

<212> DNA

<213> *Bacillus sp.*

<400>

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Met Arg Lys Lys Lys Lys Val Phe Leu Ser Val Leu Ser Ala Ala Ala

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10

15

att ttg tcg act gtt gcg tta agt aat cca tct gca ggt ggt gca agg 96

Ile Leu Ser Thr Val Ala Leu Ser Asn Pro Ser Ala Gly Gly Ala Arg

20	25	30	
aat ttt gat ctg gat ttc aaa gga att cag aca aca act gat gct aaa 144			
Asn Phe Asp Leu Asp Phe Lys Gly Ile Gln Thr Thr Thr Asp Ala Lys			
35	40	45	
ggt ttc tcc aag cag ggg cag act ggt gct gct gct ttt ctg gtg gaa 192			
Gly Phe Ser Lys Gln Gly Gln Thr Gly Ala Ala Ala Phe Leu Val Glu			
50	55	60	
tct gaa aat gtg aaa ctc cca aaa ggt ttg cag aag aag ctt gaa aca 240			
Ser Glu Asn Val Lys Leu Pro Lys Gly Leu Gln Lys Lys Leu Glu Thr			
65	70	75	80
gtc ccg gca aat aat aaa ctc cat att atc caa ttc aat gga cca att 288			
Val Pro Ala Asn Asn Lys Leu His Ile Ile Gln Phe Asn Gly Pro Ile			
85	90	95	
tta gaa gaa aca aaa cag cag ctg gaa aaa aca ggg gca aag att ctc 336			
Leu Glu Glu Thr Lys Gln Gln Leu Glu Lys Thr Gly Ala Lys Ile Leu			
100	105	110	
gac tac ata cct gat tat gct tac att gtc gag tat gag ggc gat gtt 384			
Asp Tyr Ile Pro Asp Tyr Ala Tyr Ile Val Glu Tyr Glu Gly Asp Val			
115	120	125	
aag tca gca aca agc acc att gag cac gtg gaa tcc gtg gag cct tat 432			
Lys Ser Ala Thr Ser Thr Ile Glu His Val Glu Ser Val Glu Pro Tyr			
130	135	140	
ttg ccg ata tac aga ata gat ccc cag ctt ttc aca aaa ggg gca tca 480			
Leu Pro Ile Tyr Arg Ile Asp Pro Gln Leu Phe Thr Lys Gly Ala Ser			
145	150	155	160
gag ctt gta aaa gca gtg gcg ctt gat aca aag cag aaa aat aaa gag 528			

Glu Leu Val Lys Ala Val Ala Leu Asp Thr Lys Gln Lys Asn Lys Glu
 165 170 175
 gtg caa tta aga ggc atc gaa caa atc gca caa ttc gca ata agc aat 576
 Val Gln Leu Arg Gly Ile Glu Gln Ile Ala Gln Phe Ala Ile Ser Asn
 180 185 190
 gat gtg cta tat att acg gca aag cct gag tat aag gtg atg aat gat 624
 Asp Val Leu Tyr Ile Thr Ala Lys Pro Glu Tyr Lys Val Met Asn Asp
 195 200 205
 gtt gcg cgt gga att gtc aaa gcg gat gtg gct cag agc agc tac ggg 672
 Val Ala Arg Gly Ile Val Lys Ala Asp Val Ala Gln Ser Ser Tyr Gly
 210 215 220
 ttg tat gga caa gga cag atc gta gcg gtt gcc gat aca ggg ctt gat 720
 Leu Tyr Gly Gln Gly Gln Ile Val Ala Val Ala Asp Thr Gly Leu Asp
 225 230 235 240
 aca ggt cgc aat gac agt tcg atg cat gaa gcc ttc cgc ggg aaa att 768
 Thr Gly Arg Asn Asp Ser Ser Met His Glu Ala Phe Arg Gly Lys Ile
 245 250 255
 act gca tta tat gca ttg gga cgg acg aat aat gcc aat gat acg aat 816
 Thr Ala Leu Tyr Ala Leu Gly Arg Thr Asn Asn Ala Asn Asp Thr Asn
 260 265 270
 ggt cat ggt acg cat gtg gct ggc tcc gta tta gga aac ggc tcc act 864
 Gly His Gly Thr His Val Ala Gly Ser Val Leu Gly Asn Gly Ser Thr
 275 280 285
 aat aaa gga atg gcg cct cag gcg aat cta gtc ttc caa tct atc atg 912
 Asn Lys Gly Met Ala Pro Gln Ala Asn Leu Val Phe Gln Ser Ile Met
 290 295 300

gat agc ggt ggg gga ctt gga gga cta cct tcg aat ctg caa acc tta 960
Asp Ser Gly Gly Gly Leu Gly Gly Leu Pro Ser Asn Leu Gln Thr Leu
305 310 315 320
ttc agc caa gca tac agt gct ggt gcc aga att cat aca aac tcc tgg 1008
Phe Ser Gln Ala Tyr Ser Ala Gly Ala Arg Ile His Thr Asn Ser Trp
325 330 335
gga gca gca gtg aat ggg gct tac aca aca gat tcc aga aat gtg gat 1056
Gly Ala Ala Val Asn Gly Ala Tyr Thr Thr Asp Ser Arg Asn Val Asp
340 345 350
gac tat gtg cgc aaa aat gat atg acg atc ctt ttc gct gcc ggg aat 1104
Asp Tyr Val Arg Lys Asn Asp Met Thr Ile Leu Phe Ala Ala Gly Asn
355 360 365
gaa gga ccg aac ggc gga acc atc agt gca cca ggc aca gct aaa aat 1152
Glu Gly Pro Asn Gly Gly Thr Ile Ser Ala Pro Gly Thr Ala Lys Asn
370 375 380
gca ata aca gtc gga gct acg gaa aac ctc cgc cca agc ttt ggg tct 1200
Ala Ile Thr Val Gly Ala Thr Glu Asn Leu Arg Pro Ser Phe Gly Ser
385 390 395 400
tat gcg gac aat atc aac cat gtg gca cag ttc tct tca cgt gga ccg 1248
Tyr Ala Asp Asn Ile Asn His Val Ala Gln Phe Ser Ser Arg Gly Pro
405 410 415
aca aag gat gga cgg atc aaa ccg gat gtc atg gca ccg gga acg ttc 1296
Thr Lys Asp Gly Arg Ile Lys Pro Asp Val Met Ala Pro Gly Thr Phe
420 425 430
ata cta tca gca aga tct tct ctt gca ccg gat tcc tcc ttc tgg gcg 1344
Ile Leu Ser Ala Arg Ser Ser Leu Ala Pro Asp Ser Ser Phe Trp Ala

435	440	445	
aac cat gac agt aaa tat gca tac atg ggt gga acg tcc atg gct aca 1392			
Asn His Asp Ser Lys Tyr Ala Tyr Met Gly Gly Thr Ser Met Ala Thr			
450	455	460	
ccg atc gtt gct gga aac gtg gca cag ctt cgt gag cat ttt gtg aaa 1440			
Pro Ile Val Ala Gly Asn Val Ala Gln Leu Arg Glu His Phe Val Lys			
465	470	475	480
aac aga ggc atc aca cca aag cct tct cta tta aaa gcg gca ctg att 1488			
Asn Arg Gly Ile Thr Pro Lys Pro Ser Leu Leu Lys Ala Ala Leu Ile			
485	490	495	
gcc ggt gca gct gac atc ggc ctt ggc tac ccg aac ggt aac caa gga 1536			
Ala Gly Ala Ala Asp Ile Gly Leu Gly Tyr Pro Asn Gly Asn Gln Gly			
500	505	510	
tgg gga cga gtg aca ttg gat aaa tcc ctg aac gtt gcc tat gtg aac 1584			
Trp Gly Arg Val Thr Leu Asp Lys Ser Leu Asn Val Ala Tyr Val Asn			
515	520	525	
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Glu Ser Ser Ser Leu Ser Thr Ser Gln Lys Ala Thr Tyr Ser Phe Thr			
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cct gcg agc aca act gct tcc gta acg ctt gtc aat gat ctg gac ctt 1728			
Pro Ala Ser Thr Thr Ala Ser Val Thr Leu Val Asn Asp Leu Asp Leu			
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gtc att acc gct cca aat ggc aca cag tat gta gga aat gac ttt act 1776			

Val Ile Thr Ala Pro Asn Gly Thr Gln Tyr Val Gly Asn Asp Phe Thr

580

585

590

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Ser Pro Tyr Asn Asp Asn Trp Asp Gly Arg Asn Asn Val Glu Asn Val

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taa

1923

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Ile Leu Ser Thr Val Ala Leu Ser Asn Pro Ser Ala Gly Gly Ala Arg

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Asn Phe Asp Leu Asp Phe Lys Gly Ile Gln Thr Thr Thr Asp Ala Lys
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 Gly Phe Ser Lys Gln Gly Gln Thr Gly Ala Ala Ala Phe Leu Val Glu
 50 55 60
 tct gaa aat gtg aaa ctc cca aaa ggt ttg cag aag aag ctt gaa aca 240
 Ser Glu Asn Val Lys Leu Pro Lys Gly Leu Gln Lys Lys Leu Glu Thr
 65 70 75 80
 gtc ccg gca aat aat aaa ctc cat att atc caa ttc aat gga cca att 288
 Val Pro Ala Asn Asn Lys Leu His Ile Ile Gln Phe Asn Gly Pro Ile
 85 90 95
 tta gaa gaa aca aaa cag cag ctg gaa aaa aca ggg gca aag att ctc 336
 Leu Glu Glu Thr Lys Gln Gln Leu Glu Lys Thr Gly Ala Lys Ile Leu
 100 105 110
 gac tac ata cct gat tat gct tac att gtc gag tat gag ggc gat gtt 384
 Asp Tyr Ile Pro Asp Tyr Ala Tyr Ile Val Glu Tyr Glu Gly Asp Val
 115 120 125
 aag tca gca aca agc acc att gag cac gtg gaa tcc gtg gag cct tat 432
 Lys Ser Ala Thr Ser Thr Ile Glu His Val Glu Ser Val Glu Pro Tyr
 130 135 140
 ttg ccg ata tac aga ata gat ccc cag ctt ttc aca aaa ggg gca tca 480
 Leu Pro Ile Tyr Arg Ile Asp Pro Gln Leu Phe Thr Lys Gly Ala Ser
 145 150 155 160
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 Glu Leu Val Lys Ala Val Ala Leu Asp Thr Lys Gln Lys Asn Lys Glu
 165 170 175

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 Asp Val Leu Tyr Ile Thr Ala Lys Pro Glu Tyr Lys Val Met Asn Asp
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 Val Ala Arg Gly Ile Val Lys Ala Asp Val Ala Gln Ser Ser Tyr Gly
 210 215 220
 ttg tat gga caa gga cag atc gta gcg gtt gcc gat aca ggg ctt gat 720
 Leu Tyr Gly Gln Gly Gln Ile Val Ala Val Ala Asp Thr Gly Leu Asp
 225 230 235 240
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 Thr Gly Arg Asn Asp Ser Ser Met His Glu Ala Phe Arg Gly Lys Ile
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325	330	335	
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aca aag gat gga cgg atc aaa ccg gat gtc atg gca ccg gga acg ttc 1296			
Thr Lys Asp Gly Arg Ile Lys Pro Asp Val Met Ala Pro Gly Thr Phe			
420	425	430	
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Asn His Asp Ser Lys Tyr Ala Tyr Met Gly Gly Thr Ser Met Ala Thr
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Tyr Asn Val Pro Val Gly Pro Gln Asn Phe Ser Leu Ala Ile Val Asn

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